

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/785,221A  
Source: 1FW/6  
Date Processed by STIC: 12/8/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 12/08/2006

PATENT APPLICATION: US/10/785,221A

TIME: 14:32:39

Input Set : A:\39780-1216R1C1D6 SAVED NOVEMBER 27, 2006.txt

Output Set: N:\CRF4\12082006\J785221A.raw

```

3 <110> APPLICANT: Genentech Inc.
4     Ashkenazi, Avi
5     Fong, Sherman
6     Goddard, Audrey
7     Gurney, Austin L.
8     Napier, Mary A.
9     Tumas, Daniel
10    Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
13    OF DISEASES CHARACTERIZED BY A-33 RELATED ANTIGENS
15 <130> FILE REFERENCE: P1216R1
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/785,221A
C--> 18 <141> CURRENT FILING DATE: 2004-02-24
20 <150> PRIOR APPLICATION NUMBER: US 60/066,364
21 <151> PRIOR FILING DATE: 1997-11-21
23 <150> PRIOR APPLICATION NUMBER: US 60/078,936
24 <151> PRIOR FILING DATE: 1998-03-20
26 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
27 <151> PRIOR FILING DATE: 1998-09-17
29 <160> NUMBER OF SEQ ID NOS: 30
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 299
33 <212> TYPE: PRT
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
37  Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe
38      1              5              10              15
40  Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
41              20              25              30
43  Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro
44              35              40              45
46  Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
47              50              55              60
49  Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr
50              65              70              75
52  Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
53              80              85              90
55  Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly
56              95              100             105
58  Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
59              110             115             120
61  Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
62              125             130             135

```

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```

64 Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
65           140           145           150
67 Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr
68           155           160           165
70 Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
71           170           175           180
73 Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly
74           185           190           195
76 Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
77           200           205           210
79 Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn
80           215           220           225
82 Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
83           230           235           240
85 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe
86           245           250           255
88 Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
89           260           265           270
91 Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala
92           275           280           285
94 Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
95           290           295
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 321
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
104 1           5           10           15
106 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
107           20           25           30
109 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
110           35           40           45
112 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
113           50           55           60
115 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
116           65           70           75
118 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
119           80           85           90
121 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
122           95           100          105
124 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
125           110          115          120
127 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
128           125          130          135
130 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
131           140          145          150
133 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
134           155          160          165

```

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```

136  Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
137                      170                      175                      180
139  Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
140                      185                      190                      195
142  Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe
143                      200                      205                      210
145  Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile
146                      215                      220                      225
148  Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
149                      230                      235                      240
151  Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser
152                      245                      250                      255
154  Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr
155                      260                      265                      270
157  Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe
158                      275                      280                      285
160  Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr
161                      290                      295                      300
163  Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His
164                      305                      310                      315
166  Val Tyr Glu Ala Ala Arg
167                      320

```

169 &lt;210&gt; SEQ ID NO: 3

170 &lt;211&gt; LENGTH: 390

171 &lt;212&gt; TYPE: DNA

172 &lt;213&gt; ORGANISM: Artificial Sequence

174 &lt;220&gt; FEATURE:

175 &lt;223&gt; OTHER INFORMATION: sequence is synthesized

177 &lt;400&gt; SEQUENCE: 3

```

178  cttcttgcca actggtatca ctttcaagtc cgtgacacgg gaagacactg 50
180  ggacatacac ttgtatggtc tctgaggaag gcggcaacag ctatggggag 100
182  gtcaaggtca agctcatcgt gcttgtgcct ccaccaagc ctacagttaa 150
184  catccctcc tctgccacca ttgggaaccg ggcagtgtcg acatgtcag 200
186  aacaagatgg ttccccacct tctgaataca cctgggtcaa agatgggata 250
188  gtgatgccta cgaatcccaa aagcacccgt gccttcagca actcttccta 300
190  tgtcctgaat ccacaacag gagagctggt ctttgatccc ctgtcagcct 350
192  ctgatactgg agaatacagc tgtgaggcac ggaatgggta 390

```

194 &lt;210&gt; SEQ ID NO: 4

195 &lt;211&gt; LENGTH: 726

196 &lt;212&gt; TYPE: DNA

197 &lt;213&gt; ORGANISM: Artificial Sequence

199 &lt;220&gt; FEATURE:

200 &lt;223&gt; OTHER INFORMATION: sequence is synthesized

202 &lt;400&gt; SEQUENCE: 4

```

203  tctcagtcct ctcgctgtag tcgcggagct gtgttctgtt tcccaggagt 50
205  ccttcggcgg ctgttgtgct caggtgcgcc tgatcgcat ggggacaaag 100
207  gcgcaagctc gagaggaaac tgttgtgcct cttcatattg gcgacactgt 150
209  tgtgctccct ggcattgggc agtgttacag ttgcactctt ctgaacctga 200
211  agtcagaatt cctgagaata atcctgtgaa gttgtcctgt gcctactcgg 250

```

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```

213 gcttttcttc tccccgtgtg gagtgggaagt ttgaccaagg agacaccacc 300
215 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt 350
217 gaccttcttg ccaactggta tcaccttcaa gtccgtgaca cgggaagaca 400
219 ctgggacata cacttgatg gtctctgagg aaggcggaag cagctatggg 450
221 gaggtcaagg tcaagctcat cgtgcttggt cctccatcca agcctacagt 500
223 taacatcccc tcctctgcca ccattgggaa cggggcagtg ctgacatgct 550
225 cagaacaaga tggttcccca cttctgaat acacctgggt caaagatggg 600
227 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc 650
229 ctatgtcctg aatcccacaa caggagagct ggtctttgat cccctgtcag 700
231 cctctgatac tggagaatac agctgt 726
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 1503
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: sequence is synthesized
241 <400> SEQUENCE: 5
242 gcaggcaaag taccagggcc gcctgcatgt gagccacaag gttccaggag 50
244 atgtatccct ccaattgagc accctggaga tggatgaccg gagccactac 100
246 acgtgtgaag tcacctggca gactcctgat ggcaaccaag tcgtgagaga 150
248 taagattact gagctccgtg tccagaaact ctctgtctcc aagccacag 200
250 tgacaactgg cagcgggttat ggcttcacgg tgccccaggg aatgaggatt 250
252 agccttcaat gccaggggttc ggggttctcc tcccatcagt tatatttggt 300
254 ataagcaaca gactaataac cagggaaccc atcaaagtag caaccctaag 350
256 taccttactc ttcaagcctg cggatgtagc cgactcaggc tcctatttct 400
258 gcaactgcaa gggccagggt ggctctgagc agcacagcga cattgtgaag 450
260 tttgtggtca aagactcctc aaagctactc aagaccaaga ctgaggcacc 500
262 tacaaccatg acatacccct tgaaagcaac atctacagtg aagcagtcct 550
264 gggactggac cactgacatg gatggctacc ttggagagac cagtgtctgg 600
266 ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttggt 650
268 ctgtatgggt gtttttacca tggcctatat catgctctgt cggaagacat 700
270 cccaacaaga gcatgtctac gaagcagcca gggcacatgc cagagaggcc 750
272 aacgactctg gagaaacct gaggggtggc atcttcgcaa gtggctgctc 800
274 cagtgatgag ccaacttccc agaactggg gcaacaacta ctctgatgag 850
276 ccctgcatag gacaggagta ccagatcatc gccagatca atggcaacta 900
278 cgccgcctg ctggacacag ttctctgga ttatgagttt ctggccactg 950
280 agggcaaaag tgtctgttaa aaatgcccc ttaggccagg atctgtctgac 1000
282 ataattgcct agtcagtcct tgcttctgct atggccttct tccctgctac 1050
284 ctctcttctt ggatagccca aagtgtccgc ctaccaacac tggagccgct 1100
286 gggagtcact ggctttgccc tggaaattgc cagatgcac tcagtaagc 1150
288 cagctgctgg atttggtctt gggccttctt agtatctctg ccgggggctt 1200
290 ctggtactcc tctctaaata ccagagggaa gatgcccata gcaactaggac 1250
292 ttggtcatca tgccacaga cactattcaa ctttggcac ttgccaccag 1300
294 aagacccgag gggaggctca gctctgccag ctgagaggac cagctatatc 1350
296 caggatcatt tctctttctt caggggcaga cagcttttaa ttgaaattgt 1400
298 tatttcacag gccaggggtc agttctgctc ctccactata agtctaattgt 1450
300 tctgactctc tcctggtgct caataaatat ctaatcataa cagcaaaaaa 1500
302 aaa 1503
304 <210> SEQ ID NO: 6

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## RAW SEQUENCE LISTING

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Input Set : A:\39780-1216R1C1D6 SAVED NOVEMBER 27, 2006.txt

Output Set: N:\CRF4\12082006\J785221A.raw

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305 <211> LENGTH: 319
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 6
310 Met Val Gly Lys Met Trp Pro Val Leu Trp Thr Leu Cys Ala Val
311      1          5          10          15
313 Arg Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val
314          20          25          30
316 Leu Arg Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr
317          35          40          45
319 His Thr Ser Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys
320          50          55          60
322 Leu Leu Leu Thr His Thr Glu Arg Val Val Ile Trp Pro Phe Ser
323          65          70          75
325 Asn Lys Asn Tyr Ile His Gly Glu Leu Tyr Lys Asn Arg Val Ser
326          80          85          90
328 Ile Ser Asn Asn Ala Glu Gln Ser Asp Ala Ser Ile Thr Ile Asp
329          95         100         105
331 Gln Leu Thr Met Ala Asp Asn Gly Thr Tyr Glu Cys Ser Val Ser
332         110         115         120
334 Leu Met Ser Asp Leu Glu Gly Asn Thr Lys Ser Arg Val Arg Leu
335         125         130         135
337 Leu Val Leu Val Pro Pro Ser Lys Pro Glu Cys Gly Ile Glu Gly
338         140         145         150
340 Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu Thr Cys Gln Ser Lys
341         155         160         165
343 Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys Arg Tyr Asn Ile
344         170         175         180
346 Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser Gly Gln Pro
347         185         190         195
349 Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr Tyr Ile
350         200         205         210
352 Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile Thr
353         215         220         225
355 Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
356         230         235         240
358 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile
359         245         250         255
361 Ile Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp
362         260         265         270
364 Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro
365         275         280         285
367 Glu Gln Leu Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp
368         290         295         300
370 Tyr Arg Gln Glu Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp
371         305         310         315
373 His Leu Asp Gln
376 <210> SEQ ID NO: 7
377 <211> LENGTH: 2181

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**VERIFICATION SUMMARY**

DATE: 12/08/2006

PATENT APPLICATION: US/10/785,221A

TIME: 14:32:40

Input Set : A:\39780-1216R1C1D6 SAVED NOVEMBER 27, 2006.txt

Output Set: N:\CRF4\12082006\J785221A.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date